

Application No. 10/607,077
Response dated April 18, 2008
Response to Office Action dated October 18, 2007

Amendments to the Claims are reflected in the Listing of Claims, which begins on page 3 of this paper.

Remarks begin on page 6 of this paper.

Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in this application.

Listing of Claims

Claims 1-44 (Canceled).

Claim 45 (Currently Amended). A culture-independent method of identifying determining the abundance of an environmental parameter[[s]] of interest by identifying determining the presence and abundance of [[a]] at least one nucleic acid marker sequence, wherein the abundance of the nucleic acid marker sequence(s) correlates to the abundance of the environmental parameter, comprising the steps of:

- a. providing an environmental sample containing a population of interest;
- b. isolating genomic DNA from the environmental sample;
- c. assaying the genomic DNA by utilizing [[a]] at least one pair plurality of species-specific probes to at least one of the nucleic acid marker sequences as PCR primers to determine the abundance of at least one of the nucleic acid marker sequences in the genomic DNA isolated from the sample that shows a correlation to the parameter of interest; and
- d. inferring the presence abundance of the parameter of interest based upon the presence abundance of at least one of the nucleic acid marker sequences in the genomic DNA isolated from the sample, wherein the presence of the nucleic acid marker sequence in the genomic DNA is determined using the plurality of species specific probes as PCR probes of the genomic DNA.

Claim 46 (Currently Amended). A culture-independent method of identifying determining the abundance of an environmental parameter[[s]] of interest by identifying determining the presence and abundance of [[a]] at least one nucleic acid marker sequence,

wherein the abundance of the nucleic acid marker sequence(s) correlates to the abundance of the environmental parameter, comprising the steps of:

- a. providing an environmental sample containing a population of interest;
- b. isolating genomic DNA from the environmental sample;
- c. assaying the genomic DNA by utilizing [[a]] at least one species-specific probe to at least one of the nucleic acid marker sequences as a hybridization probe to determine the abundance of at least one of the nucleic acid marker sequences in the genomic DNA isolated from the sample that shows a correlation to the parameter of interest; and
- d. inferring the presence-abundance of the parameter of interest based upon the presence-abundance of at least one of the nucleic acid marker sequences in the genomic DNA isolated from the sample, wherein the presence of the nucleic acid marker sequence in the genomic DNA is determined using the plurality of species specific probes as hybridization probes of the genomic DNA.

Claim 47 (Currently Amended). The method according to claim 45 or claim 46, wherein the abundance of at least one of the nucleic acid markers shows a perfect correlation to the abundance of the parameter of interest.

Claim 48 (Currently Amended). The method according to claim 45 or claim 46, wherein the abundance of at least one of the nucleic acid markers shows a high degree of correlation to the abundance of the parameter of interest.

Claim 49 (Currently Amended). The method according to claim 45 or claim 46, wherein the abundance of at least one of the nucleic acid markers shows a moderate degree of correlation to the abundance of the parameter of interest.

Claim 50 (Previously Presented). The method according to claim 45 or claim 46, wherein the environmental parameter of interest is a subsurface oil or natural gas deposit.

Claim 51 (Withdrawn). The method according to claim 45 or claim 46, wherein the environmental parameter of interest is a dynamic change that occurs during an oil and gas deposit's development that affect its hydrocarbon composition, migration, depletion, and hydrogen sulfide production.

Claim 52 (Withdrawn). The method according to claim 45 or claim 46, wherein the environmental parameter of interest is a mineral deposit.

Claim 53 (Withdrawn). The method according to claim 45 or claim 46, wherein the environmental parameter of interest is an indicator of the mineral deposit's composition.

Claim 54 (Withdrawn). The method according to claim 45 or claim 46, wherein the environmental parameter of interest is an agricultural pest.

Claim 55 (Withdrawn). The method according to claim 45 or claim 46, wherein the environmental parameter of interest is an industrial organic chemical.

Claim 56 (Withdrawn). The method according to claim 45 or claim 46, wherein the environmental parameter of interest is water.

Claim 57 (New). The method of claims 45 and 46, wherein the nucleic acid marker sequences are selected by a method comprising the steps of:

- a. providing a plurality of nucleic acid sequences whose abundance correlates to the abundance of the environmental parameter;

- b. ranking the nucleic acid sequences according to their level of correlation of their abundance to the abundance of the environmental parameter of interest;
- c. selecting at least one of the nucleic acid marker sequences from the set of nucleic acid sequences whose abundance has a high or moderate degree of correlation to the abundance of the environmental parameter.